

Contents

Special Issue: Computational Proteomics

Guest Editor: Mario Cannataro

Editorial

- Computational proteomics: management and analysis of proteomics data 97
Mario Cannataro
-

Papers

- Approaches to dimensionality reduction in proteomic biomarker studies 102
Melanie Hilario and Alexandros Kalousis
- Machine learning methods for predictive proteomics 119
Annalisa Barla, Giuseppe Jurman, Samantha Riccadonna, Stefano Merler, Marco Chierici and Cesare Furlanello
- Classification of mass-spectrometric data in clinical proteomics using learning vector quantization methods 129
Thomas Villmann, Frank-Michael Schleich, Markus Kostrzewa, Axel Walch and Barbara Hammer
- Algorithms and tools for analysis and management of mass spectrometry data 144
Pierangelo Veltri
- Computational methods for the comparative quantification of proteins in label-free LCⁿ-MS experiments 156
Jason W. H. Wong, Matthew J. Sullivan and Gerard Cagney
- The HUPO proteomics standards initiative—easing communication and minimizing data loss in a changing world 166
Sandra Orchard and Henning Hermjakob
-

Software Review

- Information quality in proteomics 174
David A. Stead, Norman W. Paton, Paolo Missier, Suzanne M. Embury, Cornelia Hedeler, Binling Jin, Alistair J. P. Brown and Alun Preece
-